

ABSTRACT

Methods and computer software products are provided for predicting nucleic acid hybridization affinity. In one embodiment, hybridization intensity (I) is determined using
5 the equation:

$$I = \exp\left[\sum_i P_i S_i\right]$$

where P_i is the value of the i th parameter and S_i is a value derived from the sequence of the probe. The methods and software products of the invention may be used for enhancing mutation detection, probe selection and probe array manufacturing quality
10 control.